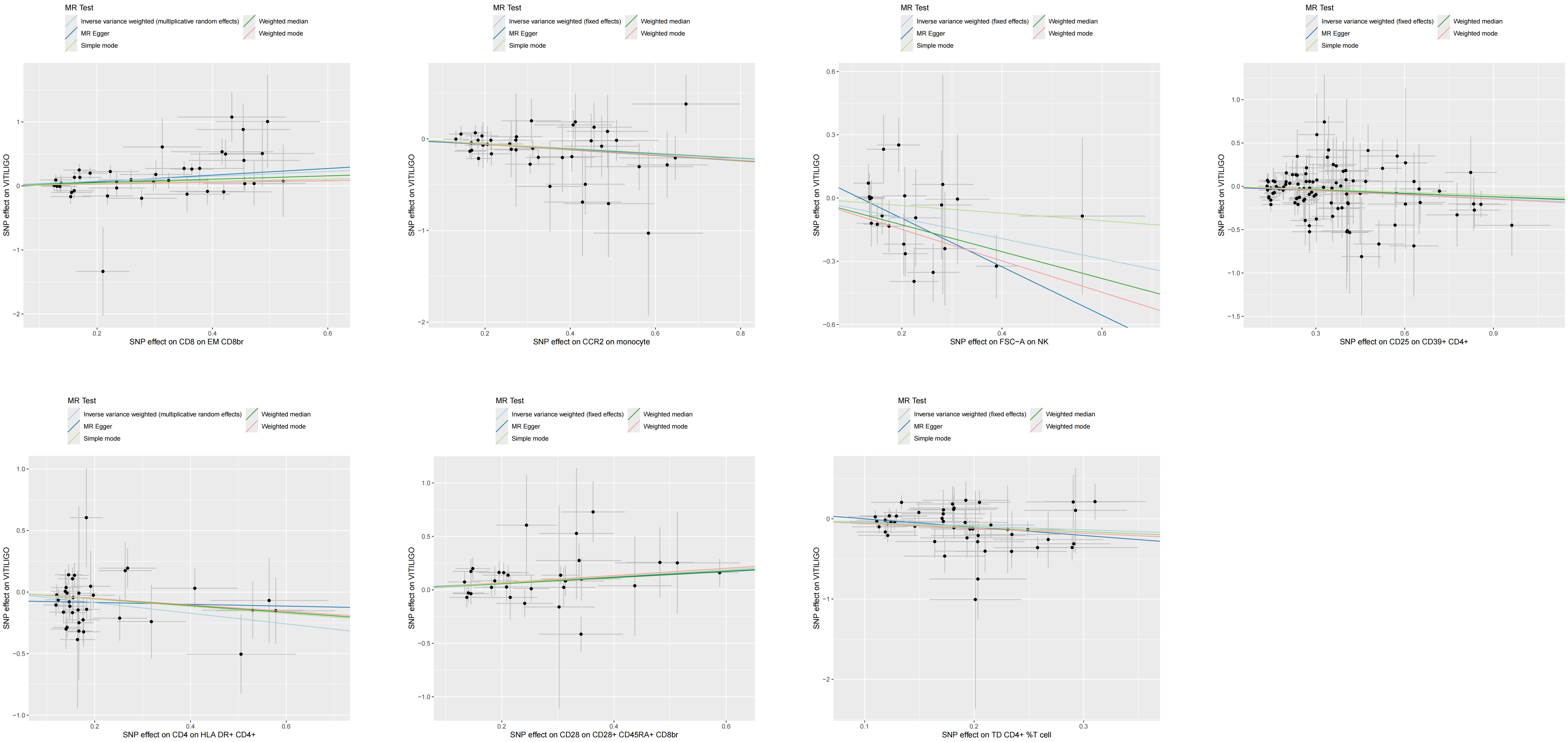
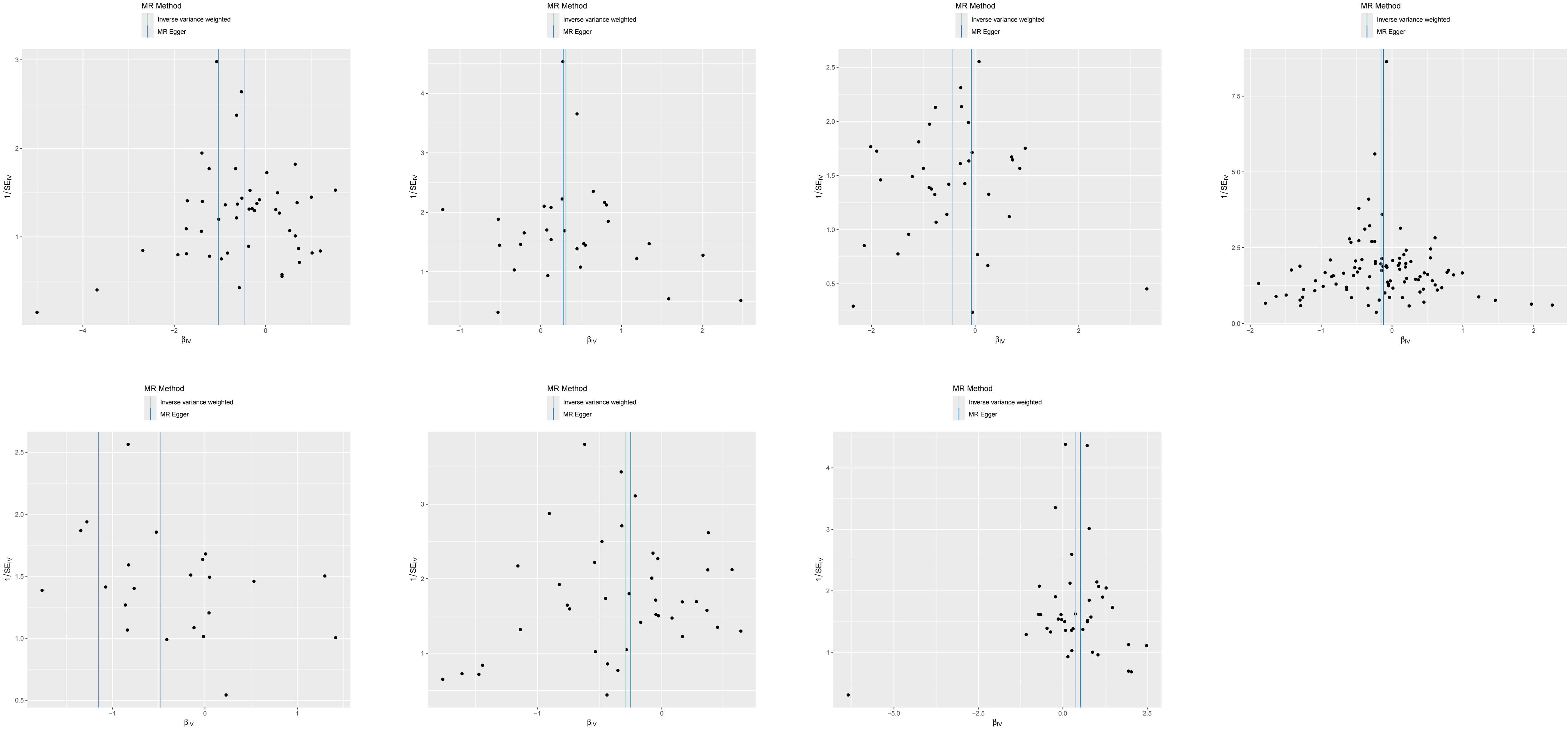


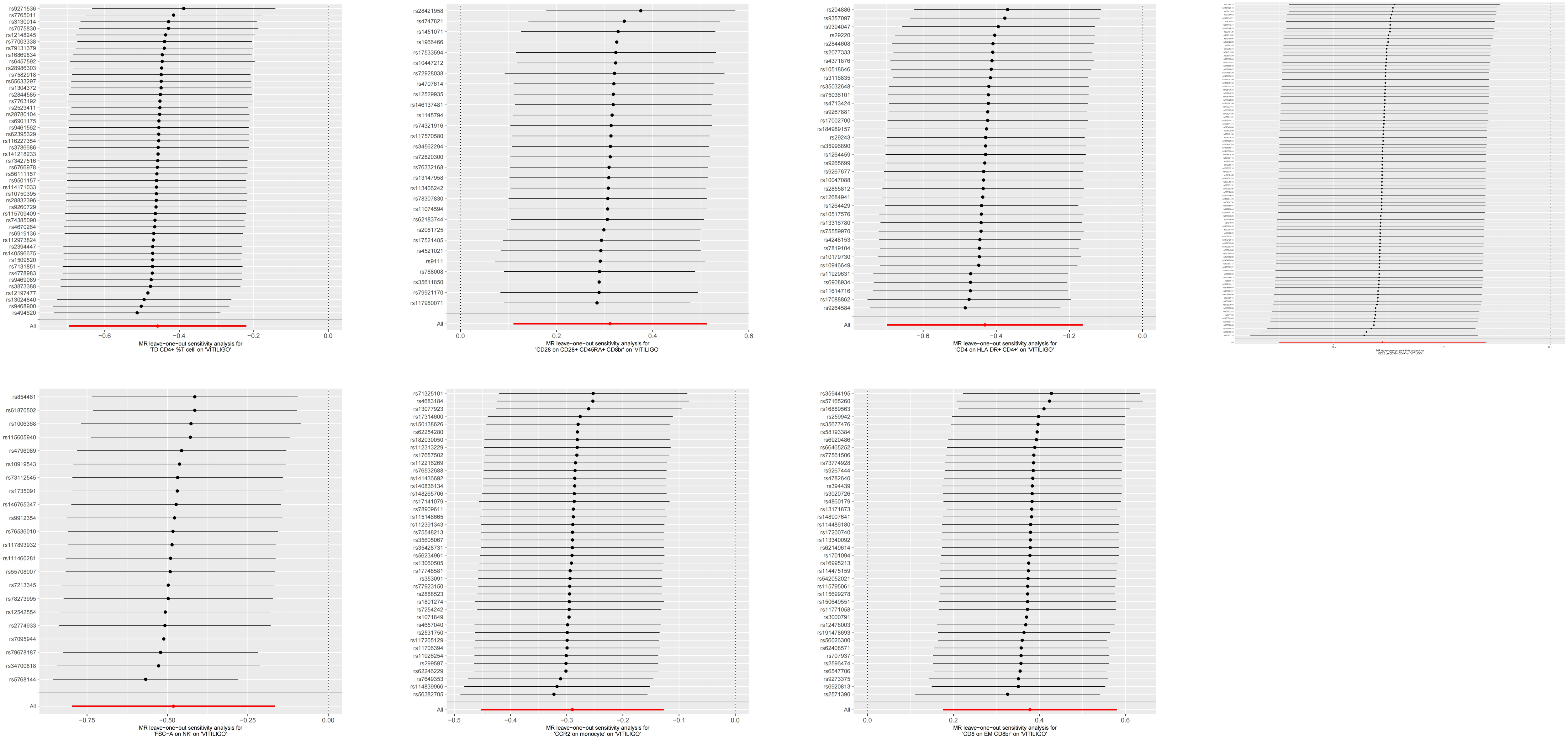
Supplementary Figure 1. Scatter plots of SNP-specific causal estimates for each exposure.

Each scatter plot presents the effect of each genetic instrument on the exposure (x-axis) against its effect on vitiligo (y-axis), with error bars representing 95% confidence intervals. The slope of the fitted line corresponds to the MR estimate (IVW method).



Supplementary Figure 2. Funnel plots for the forward MR analysis.

Each funnel plot shows the distribution of single-SNP causal estimates (x-axis: β_{IV} for each SNP) against their precision (y-axis: $1/SE_{IV}$). Symmetrical distribution around the IVW estimate suggests absence of directional pleiotropy. Plots are shown for the one significant exposure (TD $CD4^+$ %T cell) and six suggestive exposures (CD8 on EM CD8br, CCR2 on monocyte, FSC-A on NK, CD28 on $CD28^+$ $CD45RA^+$ CD8br, CD4 on HLA DR^+ $CD4^+$, CD25 on $CD39^+$ $CD4^+$).



Supplementary Figure 3 . Leave-one-out sensitivity analysis for the causal effect of immune cell phenotypes on vitiligo risk. Each plot shows the change in causal estimate (OR) for vitiligo risk after removing each single SNP one at a time. The red dotted line indicates the overall IVW estimate using all SNPs. No single SNP disproportionately altered the overall estimate, confirming robustness. Results are shown for the seven exposures with PFDR < 0.20.

Supplementary Table 1. Sensitivity analyses for forward MR: causal effects of immunophenotypes on vitiligo risk (including outlier detection).

id.exposure	id.outcome	outcome	exposure	nsnp	b_MR.Egger	se_MR.Egger	pval_MR.Egger	estimate_MR.Egger	b_Weighted.median
TDV3oU	Ic5wdw	VITILIGO	TD CD4$^+$ %T cell	47	-1.038017246	0.387606153	0.010301714	0.35 (0.17-0.76)	-0.534326046
FluSGP	vPenMO	VITILIGO	CD8 on EM CD8br	40	0.51761663	0.244824877	0.041114053	1.68 (1.04-2.71)	0.26209184
If6nSf	JhF9NT	VITILIGO	CCR2 on monocyte	40	-0.249612943	0.209219353	0.240238836	0.78 (0.52-1.17)	-0.301280619
wZTn6E	JWYTTL	VITILIGO	FSC-A on NK	22	-1.148923512	0.473672707	0.024871059	0.32 (0.13-0.80)	-0.636275839
zFDXMQ	biamAc	VITILIGO	CD25 on CD39$^+$ CD4$^+$	98	-0.120739867	0.094362675	0.203794306	0.89 (0.74-1.07)	-0.135545962
dFLMC2	razIuj	VITILIGO	CD28 on CD28$^+$ CD45RA$^+$ CD8br	29	0.278020788	0.256409354	0.287826041	1.32 (0.80-2.18)	0.283497881
rYKnET	Em901J	VITILIGO	CD4 on HLA DR$^+$ CD4$^+$	36	-0.074309395	0.355444155	0.83564841	0.93 (0.46-1.86)	-0.274946285

se_Weighted.median	pval_Weighted.median	estimate_Weighted.median	b_Inverse.variance.weighted.	se_Inverse.variance.weighted.
0.172789963	0.001985824	0.59 (0.42-0.82)	-0.458049508	0.107458913
0.142488153	0.065857269	1.30 (0.98-1.72)	0.377806389	0.103151549
0.123158053	0.014433386	0.74 (0.58-0.94)	-0.289956399	0.082895737
0.214952434	0.003075618	0.53 (0.35-0.81)	-0.481278927	0.143192423
0.078258512	0.083268514	0.87 (0.75-1.02)	-0.154943401	0.048701269
0.146409623	0.052826848	1.33 (1.00-1.77)	0.311162947	0.098163836
0.171743534	0.109396411	0.76 (0.54-1.06)	-0.431029814	0.136468104

pval_Inverse.variance.weighted.	fdr_Inverse.variance.weighted.	estimate_Inverse.variance.weighted.	b_Weighted.mode	se_Weighted.mode	pval_Weighted.mode
0.0000202	0.01477372	0.63 (0.51-0.78)	-0.603246029	0.238785364	0.015032052
0.000249635	0.091241569	1.46 (1.19-1.79)	0.137517958	0.210032681	0.516474796
0.000469034	0.114288064	0.75 (0.64-0.88)	-0.296007362	0.183761242	0.115282822
0.000776428	0.14189217	0.62 (0.47-0.82)	-0.745196045	0.328280712	0.033859243
0.001465113	0.165625823	0.86 (0.78-0.94)	-0.164822255	0.083272862	0.050616556
0.001525267	0.165625823	1.37 (1.13-1.65)	0.336032137	0.149823378	0.03300458
0.00158602	0.165625823	0.65 (0.50-0.85)	-0.259235128	0.267243075	0.338685232

estimate_Weighted.mode	b_Simple.mode	se_Simple.mode	pval_Simple.mode	estimate_Simple.mode	correct_causal_direction	steiger_pval	Value_Power
0.55 (0.34-0.87)	-0.529448328	0.361490508	0.149824518	0.59 (0.29-1.20)	TRUE	0	233766.9834
1.15 (0.76-1.73)	0.179642972	0.313409736	0.569807318	1.20 (0.65-2.21)	TRUE	0	236959.8015
0.74 (0.52-1.07)	-0.259334947	0.229331151	0.265032262	0.77 (0.49-1.21)	TRUE	0	275702.6671
0.47 (0.25-0.90)	-0.179344491	0.395426036	0.6548066	0.84 (0.39-1.81)	TRUE	4.06E-138	87607.26532
0.85 (0.72-1.00)	-0.111911325	0.141696078	0.43157203	0.89 (0.68-1.18)	TRUE	NA	-1121475.863
1.40 (1.04-1.88)	0.313681814	0.240056341	0.201945615	1.37 (0.85-2.19)	TRUE	0	229857.6837
0.77 (0.46-1.30)	-0.289743777	0.325590304	0.379594222	0.75 (0.40-1.42)	TRUE	4.14E-217	147381.0795

F	R2	Q_Inverse.variance.weighted	Q_df_Inverse.variance.weighted	Q_pval_Inverse.variance.weighted	egger_intercept	se	pval
27.75605	0.377305	58.63396223	46	0.100102412	0.103580734	0.065858	0.12277191
28.00659	0.380498	60.36066133	39	0.015674346	-0.038208778	0.060577	0.53198043
30.10652	0.416781	31.15657834	39	0.81025814	-0.011548698	0.054989	0.83477664
26.46384	0.185055	26.49392514	21	0.188238276	0.13341796	0.089352	0.15100237
48.17326	1.524417	87.45719469	97	0.745595873	-0.011899451	0.028119	0.67310612
38.98047	0.373351	30.54338623	28	0.337724793	0.008758851	0.061897	0.88851939
23.66951	0.276417	54.05257418	35	0.020845229	-0.069642949	0.064104	0.28494045

outliers	global_test_*p*
rs115625939, rs12210947, rs1632969, rs33964890	<0.001
NA	0.021
NA	0.828
NA	0.197
NA	0.769
NA	0.393
rs2596464	0.001

Notes: MR-Egger intercept *P* > 0.05 indicates no evidence of directional pleiotropy. Cochran's Q test *P* > 0.05 indicates no heterogeneity. Outlier SNPs listed were identified by MR-PRESSO global test; NA indicates no outlier detected. The global test *P* value < 0.05 suggests presence of horizontal pleiotropy. After removal of outlier SNPs, the results were re-analysed (see Supplementary Table 2).

Supplementary Table 2. Sensitivity analyses after outlier removal for exposures with detected horizontal pleiotropy.

id.exposure	id.outcome	outcome	exposure	nsnp	b_MR.Egger	se_MR.Egger	pval_MR.Egger	estimate_MR.Egger	b_Weighted.median
0H9hzq	svPvl5	VITILIGO	TD $CD4^+$ %T cell	47	-1.038017246	0.387606153	0.010301714	0.35 (0.17-0.76)	-0.534326046
YJn39C	mwEwel	VITILIGO	CD4 on HLA DR^+ $CD4^+$	36	-0.074309395	0.355444155	0.83564841	0.93 (0.46-1.86)	-0.274946285

se_Weighted.median	pval_Weighted.median	estimate_Weighted.median	b_Inverse.variance.weighted.	se_Inverse.variance.weighted.
0.176922265	0.002526766	0.59 (0.41-0.83)	-0.458049508	0.107458913
0.169839873	0.105478265	0.76 (0.54-1.06)	-0.431029814	0.136468104

pval_Inverse.variance.weighted.	fdr_Inverse.variance.weighted.	estimate_Inverse.variance.weighted.	b_Weighted.mode	se_Weighted.mode
2.02E-05	4.04E-05	0.63 (0.51-0.78)	-0.603246029	0.250095511
0.00158602	0.00158602	0.65 (0.50-0.85)	-0.259235128	0.252926108

pval_Weighted.mode	estimate_Weighted.mode	b_Simple.mode	se_Simple.mode	pval_Simple.mode	estimate_Simple.mode	correct_causal_direction
0.019909247	0.55 (0.34-0.89)	-0.529448328	0.367976302	0.156974005	0.59 (0.29-1.21)	TRUE
0.312421609	0.77 (0.47-1.27)	-0.289743777	0.333428976	0.390777147	0.75 (0.39-1.44)	TRUE

steiger_pval	Value_Power	F	R2	Q_Inverse.variance.weighted	Q_df_Inverse.variance.weighted	Q_pval_Inverse.variance.weighted
0	233766.9834	27.75605	0.377305	58.63396223	46	0.100102412
4.14E-217	147381.0795	23.66951	0.276417	54.05257418	35	0.020845229

egger_intercept	se	pval	outliers	global_test_*p*
0.103580734	0.065858	0.122772	NA	0.089
-0.069642949	0.064104	0.28494	NA	0.027

Notes: Outlier SNPs (rs115625939, rs12210947, rs1632969, rs33964890 for TD CD4$^+$ %T cell; rs2596464 for CD4 on HLA DR$^+$ CD4$^+$) were removed from the instrumental variables. After removal, the MR-PRESSO global test for TD CD4$^+$ %T cell was no longer significant ($P = 0.089$), indicating absence of residual horizontal pleiotropy. For CD4 on HLA DR$^+$ CD4$^+$, residual pleiotropy remained (global test $P = 0.027$); therefore, this suggestive association should be interpreted cautiously.